Bernhard Y Renard

List of Publications by Year
in descending order

60 papers	2,377 citations	304368 22 h-index	276539 41 g-index
85 all docs	85 docs citations	85 times ranked	3660 citing authors

#	Article	IF	Citations
1	multiFLEX-LF: A Computational Approach to Quantify the Modification Stoichiometries in Label-Free Proteomics Data Sets. Journal of Proteome Research, 2022, 21, 899-909.	1.8	1
2	Ad hoc learning of peptide fragmentation from mass spectra enables an interpretable detection of phosphorylated and cross-linked peptides. Nature Machine Intelligence, 2022, 4, 378-388.	8.3	10
3	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	9.0	133
4	ReadBouncer: precise and scalable adaptive sampling for nanopore sequencing. Bioinformatics, 2022, 38, i153-i160.	1.8	22
5	CovRadar: continuously tracking and filtering SARS-CoV-2 mutations for genomic surveillance. Bioinformatics, 2022, 38, 4223-4225.	1.8	4
6	Improving tuberculosis surveillance by detecting international transmission using publicly available whole genome sequencing data. Eurosurveillance, 2021, 26, .	3.9	9
7	Interpretable detection of novel human viruses from genome sequencing data. NAR Genomics and Bioinformatics, 2021, 3, lqab004.	1.5	33
8	MegaGO: A Fast Yet Powerful Approach to Assess Functional Gene Ontology Similarity across Meta-Omics Data Sets. Journal of Proteome Research, 2021, 20, 2083-2088.	1.8	8
9	Deep learning-based real-time detection of novel pathogens during sequencing. Briefings in Bioinformatics, 2021, 22, .	3.2	9
10	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. Nature Communications, 2021, 12, 7305.	5.8	34
11	DeePaC: predicting pathogenic potential of novel DNA with reverse-complement neural networks. Bioinformatics, 2020, 36, 81-89.	1.8	40
12	Predicting bacterial virulence factors â€" evaluation of machine learning and negative data strategies. Briefings in Bioinformatics, 2020, 21, 1596-1608.	3.2	14
13	gNOMO: a multi-omics pipeline for integrated host and microbiome analysis of non-model organisms. NAR Genomics and Bioinformatics, 2020, 2, lqaa058.	1.5	5
14	ganon: precise metagenomics classification against large and up-to-date sets of reference sequences. Bioinformatics, 2020, 36, i12-i20.	1.8	39
15	A complete and flexible workflow for metaproteomics data analysis based on MetaProteomeAnalyzer and Prophane. Nature Protocols, 2020, 15, 3212-3239.	5.5	42
16	Connecting MetaProteomeAnalyzer and PeptideShaker to Unipept for Seamless End-to-End Metaproteomics Data Analysis. Journal of Proteome Research, 2020, 19, 3562-3566.	1.8	11
17	TaxIt: An Iterative Computational Pipeline for Untargeted Strain-Level Identification Using MS/MS Spectra from Pathogenic Single-Organism Samples. Journal of Proteome Research, 2020, 19, 2501-2510.	1.8	11
18	An environment for sustainable research software in Germany and beyond: current state, open challenges, and call for action. F1000Research, 2020, 9, 295.	0.8	21

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19	Where did you come from, where did you go: Refining metagenomic analysis tools for horizontal gene transfer characterisation. PLoS Computational Biology, 2019, 15, e1007208.	1.5	9
20	Reliable variant calling during runtime of Illumina sequencing. Scientific Reports, 2019, 9, 16502.	1.6	10
21	Purple: A Computational Workflow for Strategic Selection of Peptides for Viral Diagnostics Using MS-Based Targeted Proteomics. Viruses, 2019, 11, 536.	1.5	4
22	Challenges and promise at the interface of metaproteomics and genomics: an overview of recent progress in metaproteogenomic data analysis. Expert Review of Proteomics, 2019, 16, 375-390.	1.3	86
23	Peptide-to-Protein Summarization: An Important Step for Accurate Quantification in Label-Based Proteomics. Methods in Molecular Biology, 2019, 1977, 159-180.	0.4	0
24	Computational pan-genome mapping and pairwise SNP-distance improve detection of Mycobacterium tuberculosis transmission clusters. PLoS Computational Biology, 2019, 15, e1007527.	1.5	13
25	PriLive: privacy-preserving real-time filtering for next-generation sequencing. Bioinformatics, 2018, 34, 2376-2383.	1.8	5
26	Evaluating de novo sequencing in proteomics: already an accurate alternative to database-driven peptide identification?. Briefings in Bioinformatics, 2018, 19, 954-970.	3.2	82
27	MPA Portable: A Stand-Alone Software Package for Analyzing Metaproteome Samples on the Go. Analytical Chemistry, 2018, 90, 685-689.	3.2	65
28	PAIPline: pathogen identification in metagenomic and clinical next generation sequencing samples. Bioinformatics, 2018, 34, i715-i721.	1.8	27
29	DREAM-Yara: an exact read mapper for very large databases with short update time. Bioinformatics, 2018, 34, i766-i772.	1.8	29
30	A Potential Golden Age to Come—Current Tools, Recent Use Cases, and Future Avenues for De Novo Sequencing in Proteomics. Proteomics, 2018, 18, e1700150.	1.3	43
31	seq-seq-pan: building a computational pan-genome data structure on whole genome alignment. BMC Genomics, 2018, 19, 47.	1.2	25
32	LiveKraken—real-time metagenomic classification of illumina data. Bioinformatics, 2018, 34, 3750-3752.	1.8	25
33	HiLive: real-time mapping of illumina reads while sequencing. Bioinformatics, 2017, 33, 917-319.	1.8	18
34	PaPrBaG: A machine learning approach for the detection of novel pathogens from NGS data. Scientific Reports, 2017, 7, 39194.	1.6	51
35	Critical Assessment of Metagenome Interpretation—a benchmark of metagenomics software. Nature Methods, 2017, 14, 1063-1071.	9.0	635
36	Abundance estimation and differential testing on strain level in metagenomics data. Bioinformatics, 2017, 33, i124-i132.	1.8	31

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37	MetaMeta: integrating metagenome analysis tools to improve taxonomic profiling. Microbiome, 2017, 5, 101.	4.9	36
38	SLIMM: species level identification of microorganisms from metagenomes. PeerJ, 2017, 5, e3138.	0.9	29
39	Metaproteomic data analysis at a glance: advances in computational microbial community proteomics. Expert Review of Proteomics, 2016, 13, 757-769.	1.3	67
40	Detecting horizontal gene transfer by mapping sequencing reads across species boundaries. Bioinformatics, 2016, 32, i595-i604.	1.8	23
41	DUDes: a top-down taxonomic profiler for metagenomics. Bioinformatics, 2016, 32, 2272-2280.	1.8	49
42	iPQF: a new peptide-to-protein summarization method using peptide spectra characteristics to improve protein quantification. Bioinformatics, 2016, 32, 1040-1047.	1.8	15
43	Detection of Unknown Amino Acid Substitutions Using Error-Tolerant Database Search. Methods in Molecular Biology, 2016, 1362, 247-264.	0.4	3
44	Proteomic analysis of protein carbonylation: a useful tool to unravel nanoparticle toxicity mechanisms. Particle and Fibre Toxicology, 2015, 12, 36.	2.8	49
45	Metagenomic Profiling of Known and Unknown Microbes with MicrobeGPS. PLoS ONE, 2015, 10, e0117711.	1.1	23
46	SuRankCo: supervised ranking of contigs in de novo assemblies. BMC Bioinformatics, 2015, 16, 240.	1.2	13
47	MSProGene: integrative proteogenomics beyond six-frames and single nucleotide polymorphisms. Bioinformatics, 2015, 31, i106-i115.	1.8	46
48	IPred - integrating ab initio and evidence based gene predictions to improve prediction accuracy. BMC Genomics, 2015, 16, 134.	1.2	14
49	Estimating the computational limits of detection of microbial non‒model organisms. Proteomics, 2015, 15, 3580-3584.	1.3	12
50	RAMBO-K: Rapid and Sensitive Removal of Background Sequences from Next Generation Sequencing Data. PLoS ONE, 2015, 10, e0137896.	1.1	18
51	Pipasic: similarity and expression correction for strain-level identification and quantification in metaproteomics. Bioinformatics, 2014, 30, i149-i156.	1.8	32
52	GIIRA‒RNA-Seq driven gene finding incorporating ambiguous reads. Bioinformatics, 2014, 30, 606-613.	1.8	10
53	Clock Rooting Further Demonstrates that Guinea 2014 EBOV is a Member of the Zaïre Lineage. PLOS Currents, 2014, 6, .	1.4	26
54	Analyzing genome coverage profiles with applications to quality control in metagenomics. Bioinformatics, 2013, 29, 1260-1267.	1.8	26

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55	Metagenomic abundance estimation and diagnostic testing on species level. Nucleic Acids Research, 2013, 41, e10-e10.	6.5	54
56	Overcoming Species Boundaries in Peptide Identification with Bayesian Information Criterion-driven Error-tolerant Peptide Search (BICEPS). Molecular and Cellular Proteomics, 2012, 11, M111.014167-1-M111.014167-12.	2.5	24
57	iPiG: Integrating Peptide Spectrum Matches into Genome Browser Visualizations. PLoS ONE, 2012, 7, e50246.	1.1	23
58	Computational protein profile similarity screening for quantitative mass spectrometry experiments. Bioinformatics, 2010, 26, 77-83.	1.8	16
59	Estimating the Confidence of Peptide Identifications without Decoy Databases. Analytical Chemistry, 2010, 82, 4314-4318.	3.2	23
60	When less can yield more â€" Computational preprocessing of MS/MS spectra for peptide identification. Proteomics, 2009, 9, 4978-4984.	1.3	73